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1: AF033348. Homo sapiens pota...[gi:2801451]

LOCUS AF033348 3232 bp mRNA linear PRI 21-JAN-1998
 DEFINITION Homo sapiens potassium channel (KCNQ2) mRNA, complete cds.
 ACCESSION AF033348
 VERSION AF033348.1 GI:2801451
 KEYWORDS .
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 3232)
 AUTHORS Singh,N.A., Charlier,C., Stauffer,D., DuPont,B.R., Leach,R.J.,
 Melis,R., Ronen,G.M., Bjerre,I., Quattlebaum,T., Murphy,J.V.,
 McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and
 Leppert,M.
 TITLE A novel potassium channel gene, KCNQ2, is mutated in an inherited
 epilepsy of newborns
 JOURNAL Nat. Genet. 18 (1), 25-29 (1998)
 MEDLINE 98085864
 PUBMED 9425895
 REFERENCE 2 (bases 1 to 3232)
 AUTHORS Singh,N.A., Charlier,C., Stauffer,D., DuPont,B.R., Leach,R.J.,
 Melis,R., Ronen,G.M., Bjerre,I., Quattlebaum,T., Murphy,J.V.,
 McHarg,M.L., Gagnon,D., Rosales,T.O., Peiffer,A., Anderson,V.E. and
 Leppert,M.
 TITLE Direct Submission
 JOURNAL Submitted (06-NOV-1997) Human Genetics, University of Utah, 2030E
 15N Room 2100, Salt Lake City, UT 84112, USA
 FEATURES Location/Qualifiers
 source 1..3232
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 CDS 128..2746
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 LKFARKPFCVIDIMVLIASIAVLAAGSQGNV FATSALRS LRFQLRMIRMDRRGGTW
 KLLGSVVYAHSKELVTAWYIGFLCLILASFLVYLAEKGENDHFD TYADALWNLITLT
 TIGYGD KYPQTWNGRLLAATFTLIGVSFFALPAGILGSGFALKVQE QHRQKHFEKRRN
 PAAGLIQSAWRFXATNLSRTDLHSTWQYYERTVTVP MYSSQTQTYGASRLIPPLNQLE
 LLRN LKSKSGLAFRKDP PPSKSGSPCRG P LCGCCPGRSSQKVSLKDRV FSSPRGV
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BASE COUNT 576 a 1054 c 1061 g 533 t 8 others
ORIGIN

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1681 ggatgacaag  agctgcccc  gcgagtttgt  gaccgaggac  ctgaccccg  gctcaaagt
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1861 gctgtcccg  attaagagcc  tgcagtcacg  agtgaccag  atcgtggggc  ggggcccagc
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2461 ggggaacctg  cgggacagcg  acacgtccat  ctccatcccg  tccgtggacc  acgaggagct
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2581 cagctgctac  gggcgctgg  cgccttgtgc  caaagtcagg  cctacattg  cggagggaga
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3121 acanaaggaa  gctgtncct  aagacctncc  cnaaaggcg  cctgtttggt  aagactgcgc
3181 cttggtccgg  tgggttccgg  cagcaaaagc  ggggtttgcc  gccctgtctg  tg
```

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Revised: October 24, 2001.

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Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

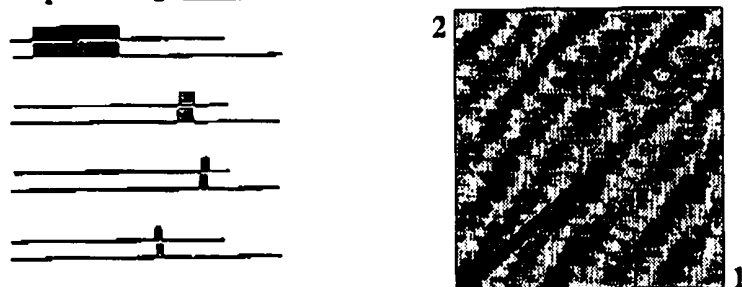
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

 Match: Mismatch: gap open: gap extension:

 x_dropoff: expect: wordsize: Filter ☒

 Sequence 1 lc1seq_1 Length 2088 (83 .. 2170) = *CDS of KCNQ4*

 Sequence 2 gi 2801451 Length 2619 (128 .. 2746) = *CDS of KCNQ2*


NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 481 bits (250), Expect = e-132

Identities = 626/814 (76%)

Strand = Plus / Plus

```

Query:          319  ctaccgcgcgcctgcagaactgggtctacaacgtgctggagcggccccgggctgggccc
                   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:          346  ctaccgcaagctgcagaatttcctctacaacgtgctggagcggccgcggcggctgggccc
potassium channel 74  Y R K L Q N F L Y N V L E R P R G W A
  
```

```

Query:          379  cgtctaccacgtcttcatatttttgggtgttccagctgcctgggtgctgtctgtgctg
                   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:          406  catctaccacgcctacgtgttctctctgggttttctctctgcctcgtgctgtctgtgtt
potassium channel 94  I Y H A Y V F L L V F S C L V L S V F
  
```

```

Query:          439  cactatccaggagcaccagggaacttgccaacgagtggtctctcatcttggaattcgtg
                   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Sbjct:          466  cactatcaaggagtatgagaagagctcggaggggggccctctacatcctggaaatcgtg
potassium channel 114  T I K E Y E K S S E G A L Y I L E I V
  
```

```

Query:          499  gatcgtgggttttcggcctggagtagatcgtccgggtctgggtccgccggatgctgctgc
                   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct:          526  tatcgtgggtgtttggcgtggagtagcttctgctgggatctgggcccaggcctgctgctgc
potassium channel 134  I V V F G V E Y F V R I W A A G C C C
  
```


Query: 1705 gttcctgggtggccaaaaggaaattcaaggagacactggcaccgtacgacgtgaaggac
 Sbjct: 1768 gttcctgggtgtccaagcggaagtccaaggagagcctggcgccctacgacgtgatggac
 potassium channel 548 F L V S K R K F K E S L R P Y D V M D

Query: 1765 cattgagcagttactcagcagggccacctggacatgctgggcccggatcaagagcctgcaa
 Sbjct: 1828 catcgagcagttactcagcggccacctggacatgctgctccgaattaagagcctgcag
 potassium channel 568 I E Q Y S A G H L D M L S R I K S L Q

Query: 1825 tcgggtggaccaaattgtgggtcgggg 1851
 Sbjct: 1888 cagagtggaccagatcgtggggcgggg 1914
 potassium channel 588 R V D Q I V G R G

Score = 60.3 bits (31), Expect = 8e-06
 Identities = 53/64 (82%)
 Strand = Plus / Plus

Query: 1921 cagcatgatgggacgcgtgggtcaagggtggagaagcaggtgcagtcctcgcagcacaag
 Sbjct: 1978 cagcatgatgggacgcgtcggaaggtggagaagcaggtcttgcctcgcagcagaag
 potassium channel 618 S M M G R L G K V E K Q V L S M E K K

Query: 1981 ggac 1984
 Sbjct: 2038 ggac 2041
 potassium channel 638 D

Score = 52.6 bits (27), Expect = 0.002
 Identities = 41/48 (85%)
 Strand = Plus / Plus

Query: 1504 cagccccaccaaggtgcaaaagagctggagcttcaatgaccgcacccg 1551
 Sbjct: 1552 cagccccagcaaggtgccaagagctggagcttcggggaccgcagccg 1599
 potassium channel 476 S P S K V P K S W S F G D R S R

CPU time: 0.12 user secs. 0.04 sys. secs 0.16 total secs.

Lambda K H
 1.33 0.621 1.12

Gapped
 Lambda K H
 1.33 0.621 1.12

Matrix: blastn matrix:i -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 21
 Number of Sequences: 0
 Number of extensions: 21

Number of successful extensions: 8
Number of sequences better than 10.0: 1
length of query: 2088
length of database: 5,708,689,566
effective HSP length: 25
effective length of query: 2063
effective length of database: 5,691,761,841
effective search space: 11742104677983
effective search space used: 11742104677983
T: 0
A: 30
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)